Utilizing the C2Maps Platform for Characterizing Drug-Protein Relations, Generating Mobile Games, and Constructing Integrated Pathway Models

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The C2Maps platform is a collection of genome-wide data that display the connections between drugs, diseases and genes. The C2Maps is used as a tool to compare and extrapolate known map data into unknown areas. By using C2Maps, researchers can compare genetic, sequential and physical information about disease specific proteins. Manual curation is important for the C2Maps platform in order to validate the literature mining approach and to overcome high levels of data noise generated from molecular networks. Currently we are examining specific drug-protein relationships in several diseases. In this research, the C-Maps website is being used to manually curate abstracts about disease specific drug-protein relations and then it is determined whether a drug “Up Regulates”, “Down Regulates”, or “Indirectly” affects a specific protein. Presently, more than 2000 specific protein-drug relations have been examined through the platform. We theorize that new drug-protein relations will be discovered through curation efforts. To broaden the scope of curation data generated, a C2Maps mobile game is in the process of being developed. This game takes advantage of novel technology in mobile development to create a game that will allow several researchers to contribute to the curation process. The data generated from the manual curation approach can be used to validate various protein-drug relationships in pharmacology and can determine the best possible drugs targeting specific proteins in cancer. Optimal drugs and their respective targets for a specific disease can then be incorporated into an integrative pathway model to analyze the mechanism of the drug. Specific properties of the drug, including chemical structure, can then be examined to determine how a specific drug acts on particular target proteins.

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